```
    -160                                                                          -73
     |          ............................                                         |
                                            ** **            *****    .....      ...|
A2   AATCTGCGAAGTGCGAGCCATTAACCACGTAAGCAAACAAACAATCTAAACCCCAAAAAAAATCTATGACTAGCCAATAGCAACCTCA
     TTAGACGCTTCACGCTCGGTAATTGGTGCATTCGTTTGTTTGTTAGATTTGGGGTTTTTTTAGATACTGATCGGTTATCGTTGGAGT
                                             *   *                *
WT1                              ---------------------------------------
m1   --------------------------------G-GTT-----G-G---------G--T-C---------------------------
m2                    -------------G-GTT-----G-G---------------C
m3                    --------------------------------G--T-C-C
m4                               --------------A-----------------T-------
WT2                                        -C-AA-CGATAA--C---------TAA-A-..-----GAATGA
```

FIG. 1

```
G CAGTGGTTCA                                                            -1000
CTTACAAGAA CCTGGTCTTC AAACCAGACA GGTTAACCAA TTCTCTCTTT AACTCTGTGT  -940
TTGGTTGCAT GTAATACTGA GAATGGAAGA CTCAAATTCT CGAGGAAATT GTTTGTTATC  -880
TGTTTCAGGG AGGCTTTGTT TGAGAAGGTC AAGAGCACAT ACAAAGACAT ATTAGGGAGC  -820
AGCTGAATCA AAGGAGGAAG AAGAAGAAGA AGAGCCTTTT TGAGGCCATT CATGAATTGG  -760
AATGAAGGAT ATCAAAAGAA TCTAACACAA AGGCCACGTC CTTCCTTCAA TCTTTCCTTC  -700
TTGTAACTAA ATAATTTTCA TCCTTTCTCT CTCTCTGTCT CTGGTCTTTT TTAGCTCAAA  -640
GTATCATCCA TTTATGTCAA AGTGTTGTAA ATTCCTCAAG ACTATATATG AGATGTTTTG  -580
TTTCATTTTC CAAAATTTCA AACTTTGTCC CCATTTAGTC TTCTACCCTT CATGCATGGT  -520
TAGCTTAGCT TAATGCTGAA CTGTTGAATA ACGATATGGG CCTTATGCTA AAAGAACAAA  -460
ACCTTATGGG TCTAAAAAAA ATAAGCCCAA TATAAAACTA TGGCCCAAAT AAGTTTAGGT  -400
CCATTAGAGT GTGAGAATAG CGCGTGTAGT GAACCGCACG AGAATGCGCG TTCGATTGTT  -340
GGTGAAGTAG TCGTCTAGAT TCCCGGGTCC ACTGATGTTT CTAGTGTATC AGACACGTGT  -280
CGACAAACTG GTGGGAGAGA TTAACGATCT TAAGTAGGTC CCACTAGATC AAGATATTAT  -220
AACGAATTGA CCTTTTTAAC CTTTCAGGTA GTCCCGGAAC TCGTGGCCTA GAATACAAAG  -160
AAGGTTGTGA ACAAGTTGAT GTTAAGATGG ACAAGAATGT AACTTGAACA AAAGCTGAAT  -100
CATCTCTTCA GCCACTAGTA TGTTGACATA TGGCAGTTTC TTTTGTAGCC TCGAAATAAA   -40
TAAATTAAAA AGTTTGAGGT TAAAGATAAT TATAGTGGCT GAGATTTCTC CATTTCCGTA    21
GCTTCTGGTC TCTTTTCTTT GTTTCATTGA TCAAAAGCAA ATCACTTCTT CTTCTTCTTC    81
TTCTCGATTT CTTACTGTTT TCTTATCCAA CGAAATCTGG AATTAAAAAT GGAATCTTTA   141
TCGAATCCAA GCTGATTTTG TTTCTTTCAT TGAATCATCT CTCTAAAGGT ACTTAAGATT   201
GATTTATTGT CATGGTCTTT CTTATTGTTT GATGAATAAC TTGACTTGAT TGTTTTTTGT   261
TTTGTGGATT AGTGGAATTT TGTAAAGAGA AGATCTGAAG TTGTGTAGAG GAGCTTAGTG   321
ATG GAG ACA AAT TCG TCT GGA GAA GAT CTG GTT ATT AAG GTAAATTAAC      370
```

FIG. 2A

```
Met Glu Thr Asn Ser Ser Gly Glu Asp Leu Val Ile Lys
 1               5                   10
TAAATTTTAG GGGGAAGATG ATTGTTTTAG GTGTCAAAGA TTGAGAATTT TAATGAAACT      430
TGATATAG ACT CGG AAG CCA TAT ACG ATA ACA AAG CAA CGT GAA AGG TGG      480
         Thr Arg Lys Pro Tyr Thr Ile Thr Lys Gln Arg Glu Arg Trp
             15                  20                  25
ACT GAG GAA GAA CAT AAT AGA TTC ATT GAA GCT TTG AGG CTT TAT GGT      528
Thr Glu Glu Glu His Asn Arg Phe Ile Glu Ala Leu Arg Leu Tyr Gly
         30                  35                  40
AGA GCA TGG CAG AAG ATT GAA G GTTGATTTTT ATTTCCCTTT ATATGTCTTA      580
Arg Ala Trp Gln Lys Ile Glu
     45                  50
TTTTTTGTGT TTGCAGAGGT TTGTCTTCAA ACTGATTTGC TTTTTTTCAT TTGGACAG      638
 AA CAT GTA GCA ACA AAA ACT GCT GTC CAG ATA AGA AGT CAC GCT CAG      685
Glu His Val Ala Thr Lys Thr Ala Val Gln Ile Arg Ser His Ala Gln
                 55                  60                  65
AAA TTT TTC TCC AAG GTAAAATCGG TTAATTTTGA AATGATGTTC TCATCTTCAT      740
Lys Phe Phe Ser Lys
             70
TGGCTTAATG CTTAAGACTT ATTGAAAGCC AGGCAAGTTT TCTGCTTCTT TTGCTTCTTA      800
GTCAGGAGAT AGATAGATTA CGTTTTTAGA GTTTAGTAAT GAGCAATAAG TCTTAAAATA      860
GTTGGAGAAA TGACGAGATG TAATCGTTTT CTTTTGTTTA TGCCTATATC TTGTTAATCC      920
ACAAACATGT ACATAGATTC TTCAGAAGAA TGTTAGTTTC TTTAGATTCT TCAGATAAAC      980
TTGTGTCTTC TTACCGATTC TGAGGTAGTG GCAAAAGTGG GCTGAGTGCT AGAAATTTTT     1040
```

FIG. 2B

```
GAATGTTCCT TGTGATAAGC CATAGAGGTA AACCATTTTT GATTTTCCAG TTCTGTCATT   1100
TAAACTTGTT AGGTGTCATT AGATTTTTGT TTGTTTACGT TTGTTTAGAG GGTAACAAAA   1160
CTACTCTCAT CTCTCTCAG GTA GAG AAA GAG GCT GAA GCT AAA GGT GTA GCT    1212
                     Val Glu Lys Glu Ala Glu Ala Lys Gly Val Ala
                                  75                  80
ATG GGT CAA GCG CTA GAC ATA GCT ATT CCT CCT CCA CGG CCT AAG CGT     1260
Met Gly Gln Ala Leu Asp Ile Ala Ile Pro Pro Pro Arg Pro Lys Arg
        85                  90                  95
AAA CCA AAC AAT CCT TAT CCT CGA AAG ACG GGA AGT GGA ACG ATC CTT     1308
Lys Pro Asn Asn Pro Tyr Pro Arg Lys Thr Gly Ser Gly Thr Ile Leu
    100                 105                 110
ATG TCA AAA ACG GGT GTG AAT GAT GGA AAA GAG TCC CTT GGA TCA GAA     1356
Met Ser Lys Thr Gly Val Asn Asp Gly Lys Glu Ser Leu Gly Ser Glu
115                 120                 125                 130
AAA GTG TCG CAT CCT GAG GTGATTTTCA TGGTCATATG GCATCTTTTT GCAGTGTGTC 1414
Lys Val Ser His Pro Glu
                135
ACATTGCTCC TCATGTTATT AATACAGATT GTGTGCTTCG TTTATAG ATG GCC AAT     1470
                                                    Met Ala Asn
GAA GAT CGA CAA CAA TCA AAG CCT GAA GAG AAA ACT CTG CAG GAA GAC     1518
Glu Asp Arg Gln Gln Ser Lys Pro Glu Glu Lys Thr Leu Gln Glu Asp
140                 145                 150                 155
```

FIG. 2C

```
AAC TGT TCA GAT TGT TTC ACT CAT CAG TAT CTC TCT GCT GCA TCC TCC      1566
Asn Cys Ser Asp Cys Phe Thr His Gln Tyr Leu Ser Ala Ala Ser Ser
                160                 165                 170
ATG AAT AAA AGT TGT ATA GAG ACA TCA AAC GCA AGC ACT TTC CGC GAG      1614
Met Asn Lys Ser Cys Ile Glu Thr Ser Asn Ala Ser Thr Phe Arg Glu
            175                 180                 185
TTC TTG CCT TCA CGG GAA GAG GTAAAAAACA ATCTTTCATT GCTATTTGAG         1665
Phe Leu Pro Ser Arg Glu Glu
        190
GTTTTAAGAC GATTAGTACT TTTCATGAAA CTAAAACCGT GGGGGAATAA CAG GGA       1721
                                                           Gly
                                                           195
AGT CAG AAT AAC AGG GTA AGA AAG GAG TCA AAC TCA GAT TTG AAT GCA      1769
Ser Gln Asn Asn Arg Val Arg Lys Glu Ser Asn Ser Asp Leu Asn Ala
                200                 205                 210
AAA TCT CTG GAA AAC GGT AAT GAG CAA GGA CCT CAG ACT TAT CCG ATG      1817
Lys Ser Leu Glu Asn Gly Asn Glu Gln Gly Pro Gln Thr Tyr Pro Met
            215                 220                 225
CAT ATC CCT GTG CTA GTG CCA TTG GGG AGC TCA ATA ACA AGT TCT CTA      1865
His Ile Pro Val Leu Val Pro Leu Gly Ser Ser Ile Thr Ser Ser Leu
        230                 235                 240
TCA CAT CCT CCT TCA GAG CCA GAT AGT CAT CCC CAC ACA GTT GCA GGA      1913
Ser His Pro Pro Ser Glu Pro Asp Ser His Pro His Thr Val Ala Gly
    245                 250                 255
```

FIG. 2D

```
GAT TAT CAG TCG TTT CCT AAT CAT ATA ATG TCA ACC CTT TTA CAA ACA      1961
Asp Tyr Gln Ser Phe Pro Asn His Ile Met Ser Thr Leu Leu Gln Thr
260                 265                 270                 275
CCG GCT CTT TAT ACT GCC GCA ACT TTC GCC TCA TCA TTT TGG CCT CCC      2009
Pro Ala Leu Tyr Thr Ala Ala Thr Phe Ala Ser Ser Phe Trp Pro Pro
                280                 285                 290
GAT TCT AGT GGT GGC TCA CCT GTT CCA GGG AAC TCA CCT CCG AAT CTG      2057
Asp Ser Ser Gly Gly Ser Pro Val Pro Gly Asn Ser Pro Pro Asn Leu
            295                 300                 305
GCT GCC ATG GCC GCA GCC ACT GTT GCA GCT GCT AGT GCT TGG TGG GCT      2105
Ala Ala Met Ala Ala Ala Thr Val Ala Ala Ala Ser Ala Trp Trp Ala
        310                 315                 320
GCC AAT GGA TTA TTA CCT TTA TGT GCT CCT CTT AGT TCA GGT GGT TTC      2153
Ala Asn Gly Leu Leu Pro Leu Cys Ala Pro Leu Ser Ser Gly Gly Phe
    325                 330                 335
ACT AGT CAT CCT CCA TCT ACT TTT GGA CCA TCA TGT GAT GTA GAG TAC      2201
Thr Ser His Pro Pro Ser Thr Phe Gly Pro Ser Cys Asp Val Glu Tyr
340                 345                 350                 355
ACA AAA GCA AGC ACT TTA CAA CAT GGT TCT GTG CAG AGC CGA GAG CAA      2249
Thr Lys Ala Ser Thr Leu Gln His Gly Ser Val Gln Ser Arg Glu Gln
                360                 365                 370
GAA CAC TCC GAG GCA TCA AAG GCT CGA TCT TCA CTG GAC TCA GAG GAT      2297
Glu His Ser Glu Ala Ser Lys Ala Arg Ser Ser Leu Asp Ser Glu Asp
            375                 380                 385
```

FIG. 2E

```
GTT GAA AAT AAG AGT AAA CCA GTT TGT CAT GAG CAG CCT TCT GCA ACA      2345
Val Glu Asn Lys Ser Lys Pro Val Cys His Glu Gln Pro Ser Ala Thr
        390                 395                 400
CCT GAG AGT GAT GCA AAG GGT TCA GAT GGA GCA GGA GAC AGA AAA CAA      2393
Pro Glu Ser Asp Ala Lys Gly Ser Asp Gly Ala Gly Asp Arg Lys Gln
    405                 410                 415
GTT GAC CGG TCC TCG TGT GGC TCA AAC ACT CCG TCG AGT AGT GAT GAT      2441
Val Asp Arg Ser Ser Cys Gly Ser Asn Thr Pro Ser Ser Ser Asp Asp
420                 425                 430                 435
GTT GAG GCG GAT GCA TCA GAA AGG CAA GAG GAT GGC ACC AAT GGT GAG      2489
Val Glu Ala Asp Ala Ser Glu Arg Gln Glu Asp Gly Thr Asn Gly Glu
                440                 445                 450
GTG AAA GAA ACG AAT GAA GAC ACT AAT AAA CCT CAA ACT TCA GAG TCC      2537
Val Lys Glu Thr Asn Glu Asp Thr Asn Lys Pro Gln Thr Ser Glu Ser
            455                 460                 465
AAT GCA CGC CGC AGT AGA ATC AGC TCC AAT ATA ACC GAT CCA TGG AAG      2585
Asn Ala Arg Arg Ser Arg Ile Ser Ser Asn Ile Thr Asp Pro Trp Lys
        470                 475                 480
TCT GTG TCT GAC GAG GTACTTACTT GGACTAAAGA TCAACTTCCT TTATTTCAAA      2640
Ser Val Ser Asp Glu
    485
TCATTTTCTC ATATAAATAT TGTACATTCG GGT CGA ATT GCC TTC CAA GCT CTC     2694
                                 Gly Arg Ile Ala Phe Gln Ala Leu
                                     490                 495
```

FIG. 2F

```
TTC TCC AGA GAG GTA TTG CCG CAA AGT TTT ACA TAT CGA GAA GAA CAC     2742
Phe Ser Arg Glu Val Leu Pro Gln Ser Phe Thr Tyr Arg Glu Glu His
            500                 505                 510
AGA GAG GAA GAA CAA CAA CAA CAA GAA CAA AGA TAT CCA ATG GCA CTT     2790
Arg Glu Glu Glu Gln Gln Gln Gln Glu Gln Arg Tyr Pro Met Ala Leu
        515                 520                 525
GAT CTT AAC TTC ACA GCT CAG TTA ACA CCA GTT GAT GAT CAA GAG GAG     2838
Asp Leu Asn Phe Thr Ala Gln Leu Thr Pro Val Asp Asp Gln Glu Glu
    530                 535                 540
AAG AGA AAC ACA GGA TTT CTT GGA ATC GGA TTA GAT GCT TCA AAG CTA     2886
Lys Arg Asn Thr Gly Phe Leu Gly Ile Gly Leu Asp Ala Ser Lys Leu
545                 550                 555                 560
ATG AGT AGA GGA AGA ACA GGT TTT AAA CCA TAC AAA AGA TGT TCC ATG     2934
Met Ser Arg Gly Arg Thr Gly Phe Lys Pro Tyr Lys Arg Cys Ser Met
                565                 570                 575
GAA GCC AAA GAA AGT AGA ATC CTC AAC AAC AAT CCT ATC ATT CAT GTG     2982
Glu Ala Lys Glu Ser Arg Ile Leu Asn Asn Asn Pro Ile Ile His Val
            580                 585                 590
GAA CAG AAA GAT CCC AAA CGG ATG CGG TTG GAA ACT CAA GCT TCC ACA     3030
Glu Gln Lys Asp Pro Lys Arg Met Arg Leu Glu Thr Gln Ala Ser Thr
        595                 600                 605
TGAGACTCTA TTTTCATCTG ATCTGTTGTT TGTACTCTGT TTTTAAGTTT TCAAGACCAC   3090
TGCTACATTT TCTTTTTCTT TTGAGGCCTT TGTATTTGTT TCCTTGTCCA TAGTCTTCCT   3150
GTAACATTTG ACTCTGTATT ATTCAACAAA TCATAAACTG TTTAATCTTT TTTTTTCCAA   3210
CCTGGAAAGA ACTTCACTCA AGGGGCTCTT GTTCTTGATA TATGCAAACG ACAGAGTTCC   3270
AAAACGTAAT CTTAGCCCAT CCATCACCCT TAAGTTGTCT CATAACTCAT AAGTAAGCAC   3330
AAAA
```

FIG. 2G

```
           *                             *                             *                   aa
CCA1   RERWTEEEHNRFIEALRLYGR-AWQKIEEH-VATKTAVQIRSHAQKFF-SKVEKE  75
St1    GVPWTEEEHRMFLLGLGKLGKGDWRGIARNYVISRTPTQVASHAQKYFIRQSNMS 155
HMyb   KTSWTEEEDRIIYQAHKRLGN-RWAEIAKL-LPGRTDNAIKNHWNSTMRRKVEQE 196
CMyb   KTSWTEEEDRIIYQAHKRLGN-RWAEIAKL-LPGRTDNAIKNHWNSTMRRKVEQE 196
DMyb   KTAWTEKEDEIIYQAHLELGN-QWAKIAKR-LPGRTDNAIKNHWNSTMRRKYDVE 240
ZmC1   RGNISYDEEDLIIRLHRLYGN-RWSLIAGR-LPGRTDNEIKNYWNSTLGRRAGAG 121
YBAS1  LREWTLEEDLNLISKVKAYGT-KWRKISSE-MEFRPSLTCRNRWRKII-TMVVRG 220
AtG11  KGNFTEQEEDLIIRLHKLLGN-RWSLIAKR-VPGRTDNQVKNYWNTHL-SKKLVG 120
```

FIG. 3

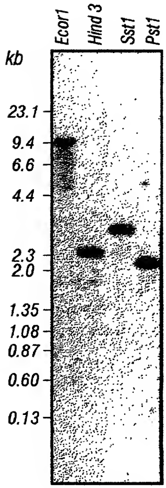

Ecor1
Hind 3
Sst1
Pst1
kb
23.1
9.4
6.6
4.4
2.3
2.0
1.35
1.08
0.87
0.60
0.13

FIG. 4

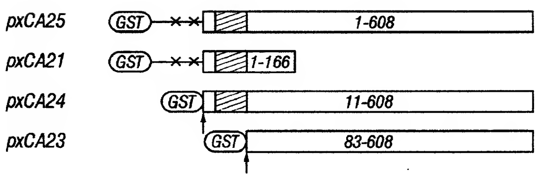

pxCA25
GST
1-608
pxCA21
GST
1-166
pxCA24
GST
11-608
pxCA23
GST
83-608

FIG. 5

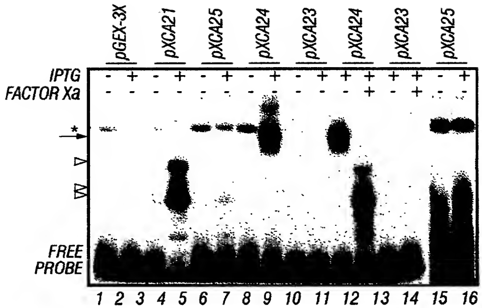

pGEX-3X
pXCA21
pXCA25
pXCA24
pXCA23
pXCA24
pXCA23
pXCA25
IPTG - + - + - + - + - + + + + + - +
FACTOR Xa - - - - - - - - - - - + - + - -
*
FREE
PROBE
1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16

FIG. 6

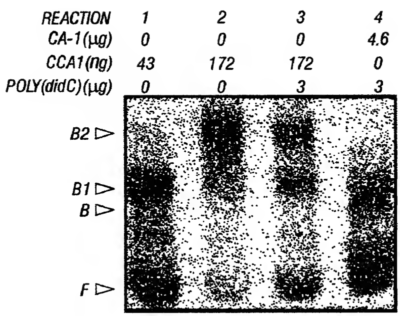

REACTION 1 2 3 4
CA-1 (μg) 0 0 0 4.6
CCA1 (ng) 43 172 172 0
POLY(didC) (μg) 0 0 3 3
B2
B1
B
F

FIG. 7A

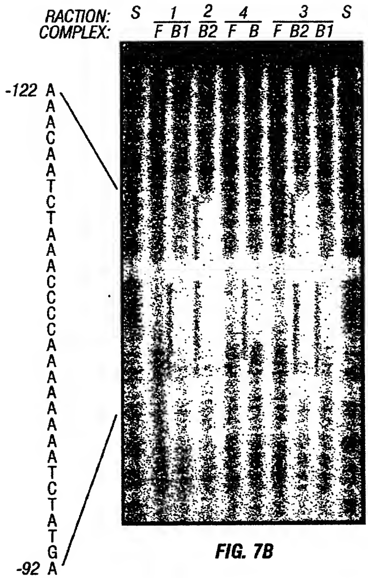

RACTION: S 1 2 4 3 S
COMPLEX: F B1 B2 F B F B2 B1
-122 A
A
A
C
A
A
T
C
T
A
A
A
C
C
C
C
A
A
A
A
A
A
A
A
T
C
T
A
T
G
-92 A

FIG. 7B

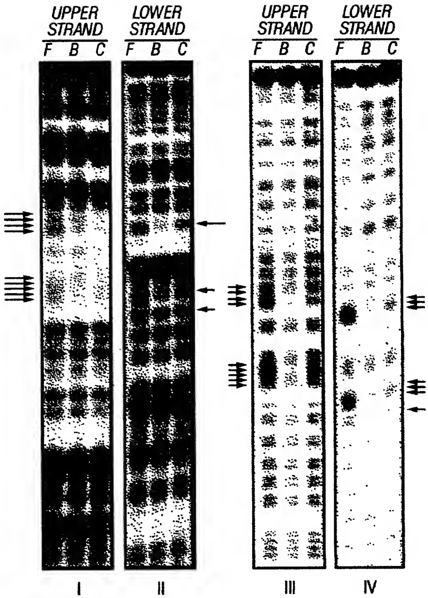

UPPER STRAND
F B C
LOWER STRAND
F B C
UPPER STRAND
F B C
LOWER STRAND
F B C
I
II
III
IV

FIG. 8

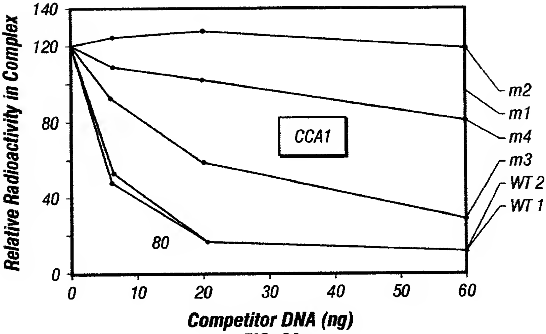

Relative Radioactivity in Complex
140
120
80
40
0
0
10
20
30
40
50
60
CCA1
80
m2
m1
m4
m3
WT 2
WT 1
Competitor DNA (ng)

FIG. 9A

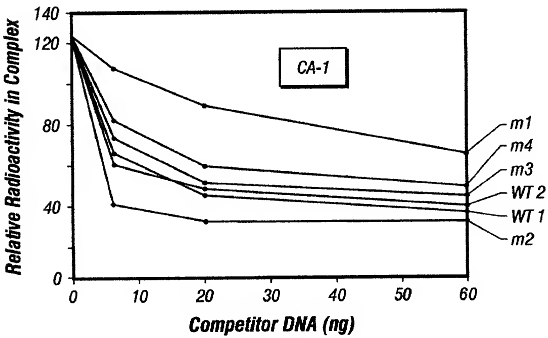

Relative Radioactivity in Complex
140
120
80
40
0
0
10
20
30
40
50
60
CA-1
m1
m4
m3
WT 2
WT 1
m2
Competitor DNA (ng)

FIG. 9B

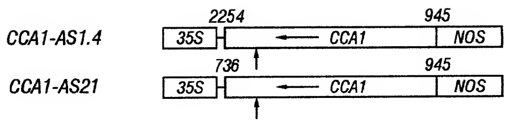

CCA1-AS1.4
2254
945
35S
CCA1
NOS
CCA1-AS21
736
945
35S
CCA1
NOS

FIG. 10

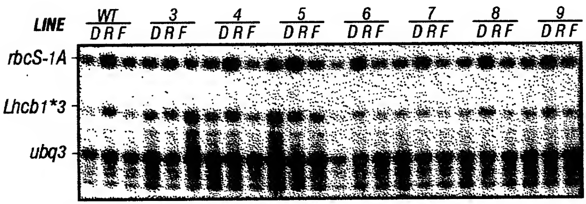

LINE
WT
3
4
5
6
7
8
9
D R F
rbcS-1A
Lhcb1*3
ubq3

FIG. 11

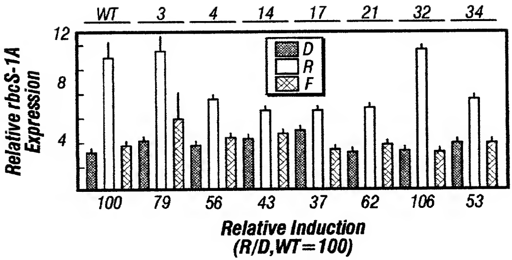


FIG. 11A

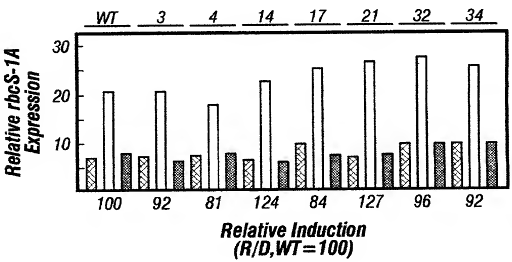


FIG. 11B

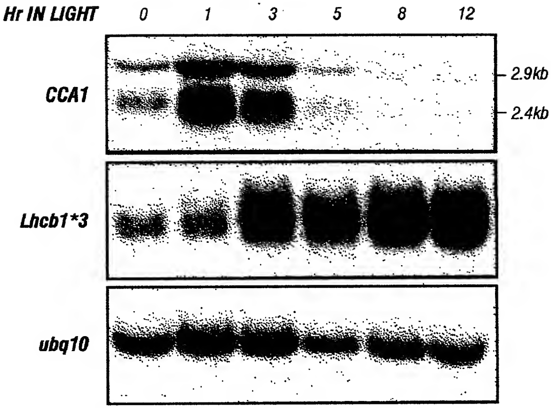


FIG. 12A

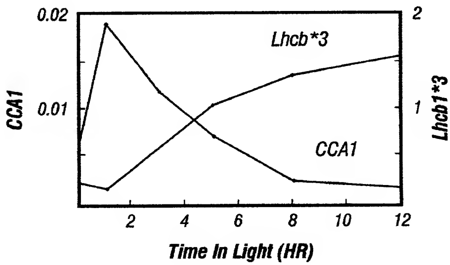


FIG. 12B

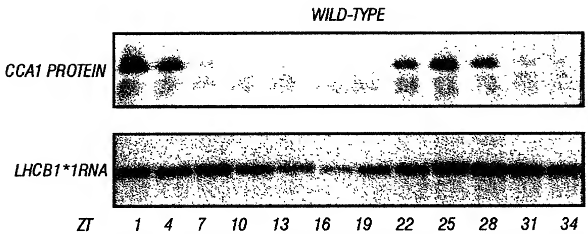


FIG. 13A

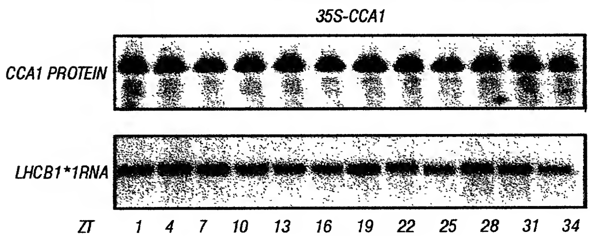
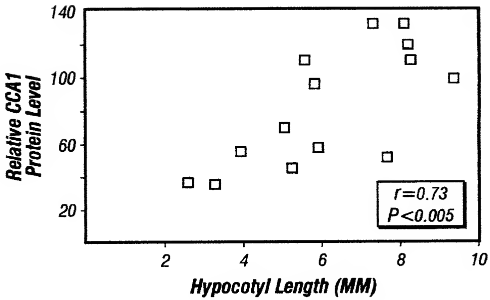
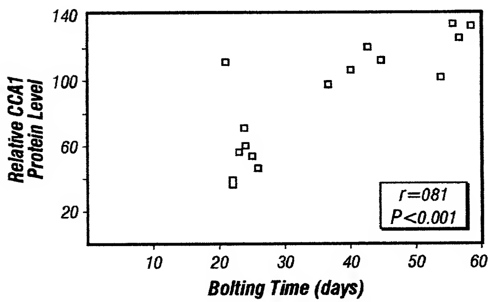


FIG. 13B



140
100
60
20
Relative CCA1 Protein Level
2
4
6
8
10
Hypocotyl Length (MM)
r=0.73
P<0.005

FIG. 14



140
100
60
20
Relative CCA1 Protein Level
10
20
30
40
50
60
Bolting Time (days)
r=081
P<0.001

FIG. 15